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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/882,774

DATE: 07/05/2001

TIME: 11:25:37

Input Set : A:\003592-007.ST25.txt

Output Set: N:\CRF3\07052001\I882774.raw

4 <110> APPLICANT: Houston, Michael E.  
 5 Hodges, Robert  
 7 <120> TITLE OF INVENTION: Use of Coiled-Coil Structural Scaffold to Generate  
 8 Structure-Specific Peptides  
 10 <130> FILE REFERENCE: 003592-007  
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/882,774  
 C--> 12 <141> CURRENT FILING DATE: 2001-06-14  
 12 <150> PRIOR APPLICATION NUMBER: US 60/211,892  
 13 <151> PRIOR FILING DATE: 2000-06-14  
 15 <150> PRIOR APPLICATION NUMBER: US 60/213,387  
 16 <151> PRIOR FILING DATE: 2000-06-23  
 18 <160> NUMBER OF SEQ ID NOS: 16  
 20 <170> SOFTWARE: PatentIn version 3.0  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 619  
 24 <212> TYPE: PRT  
 25 <213> ORGANISM: Streptococcus pneumoniae  
 27 <400> SEQUENCE: 1  
 29 Met Asn Lys Lys Lys Met Ile Leu Thr Ser Leu Ala Ser Val Ala Ile  
 30 1 5 10 15  
 32 Leu Gly Ala Gly Phe Val Ala Ser Gln Pro Thr Val Val Arg Ala Glu  
 33 20 25 30  
 35 Glu Ser Pro Val Ala Ser Gln Ser Lys Ala Glu Lys Asp Tyr Asp Ala  
 36 35 40 45  
 38 Ala Lys Lys Asp Ala Lys Asn Ala Lys Lys Ala Val Glu Asp Ala Gln  
 39 50 55 60  
 41 Lys Ala Leu Asp Asp Ala Lys Ala Ala Gln Lys Lys Tyr Asp Glu Asp  
 42 65 70 75 80  
 44 Gln Lys Lys Thr Glu Glu Lys Ala Ala Leu Glu Lys Ala Ala Ser Glu  
 45 85 90 95  
 47 Glu Met Asp Lys Ala Val Ala Ala Val Gln Gln Ala Tyr Leu Ala Tyr  
 48 100 105 110  
 50 Gln Gln Ala Thr Asp Lys Ala Ala Lys Asp Ala Ala Asp Lys Met Ile  
 51 115 120 125  
 53 Asp Glu Ala Lys Lys Arg Glu Glu Glu Ala Lys Thr Lys Phe Asn Thr  
 54 130 135 140  
 56 Val Arg Ala Met Val Val Pro Glu Pro Glu Gln Leu Ala Glu Thr Lys  
 57 145 150 155 160  
 59 Lys Lys Ser Glu Glu Ala Lys Gln Lys Ala Pro Glu Leu Thr Lys Lys  
 60 165 170 175  
 62 Leu Glu Glu Ala Lys Ala Lys Leu Glu Glu Ala Glu Lys Lys Ala Thr  
 63 180 185 190  
 65 Glu Ala Lys Gln Lys Val Asp Ala Glu Glu Val Ala Pro Gln Ala Lys  
 66 195 200 205  
 68 Ile Ala Glu Leu Glu Asn Gln Val His Arg Leu Glu Gln Glu Leu Lys  
 69 210 215 220  
 71 Glu Ile Asp Glu Ser Glu Ser Glu Asp Tyr Ala Lys Glu Gly Phe Arg

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```

72 225          230          235          240
74 Ala Pro Leu Gln Ser Lys Leu Asp Ala Lys Lys Ala Lys Leu Ser Lys
75          245          250          255
77 Leu Glu Glu Leu Ser Asp Lys Ile Asp Glu Leu Asp Ala Glu Ile Ala
78          260          265          270
80 Lys Leu Glu Asp Gln Leu Lys Ala Ala Glu Glu Asn Asn Asn Val Glu
81          275          280          285
83 Asp Tyr Phe Lys Glu Gly Leu Glu Lys Thr Ile Ala Ala Lys Lys Ala
84          290          295          300
86 Glu Leu Glu Lys Thr Glu Ala Asp Leu Lys Lys Ala Val Asn Glu Pro
87 305          310          315          320
89 Glu Lys Pro Ala Pro Ala Pro Glu Thr Pro Ala Pro Glu Ala Pro Ala
90          325          330          335
92 Glu Gln Pro Lys Pro Ala Pro Ala Pro Gln Pro Ala Pro Ala Pro Lys
93          340          345          350
95 Pro Glu Lys Pro Ala Glu Gln Pro Lys Pro Glu Lys Thr Asp Asp Gln
96          355          360          365
98 Gln Ala Glu Glu Asp Tyr Ala Arg Arg Ser Glu Glu Glu Tyr Asn Arg
99          370          375          380
101 Leu Thr Gln Gln Gln Pro Pro Lys Ala Glu Lys Pro Ala Pro Ala Pro
102 385          390          395          400
104 Lys Thr Gly Trp Lys Gln Glu Asn Gly Met Trp Tyr Phe Tyr Asn Thr
105          405          410          415
107 Asp Gly Ser Met Ala Thr Gly Trp Leu Gln Asn Asn Gly Ser Trp Tyr
108          420          425          430
110 Tyr Leu Asn Ser Asn Gly Ala Met Ala Thr Gly Trp Leu Gln Tyr Asn
111          435          440          445
113 Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ala Met Ala Thr Gly Trp
114          450          455          460
116 Ala Lys Val Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ala Met
117 465          470          475          480
119 Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser Trp Tyr Tyr Leu Asn Ala
120          485          490          495
122 Asn Gly Ala Met Ala Thr Gly Trp Ala Lys Val Asn Gly Ser Trp Tyr
123          500          505          510
125 Tyr Leu Asn Ala Asn Gly Ala Met Ala Thr Gly Trp Leu Gln Tyr Asn
126          515          520          525
128 Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ala Met Ala Thr Gly Trp
129          530          535          540
131 Ala Lys Val Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ala Met
132 545          550          555          560
134 Ala Thr Gly Trp Val Lys Asp Gly Asp Thr Trp Tyr Tyr Leu Glu Ala
135          565          570          575
137 Ser Gly Ala Met Lys Ala Ser Gln Trp Phe Lys Val Ser Asp Lys Trp
138          580          585          590
140 Tyr Tyr Val Asn Gly Leu Gly Ala Leu Ala Val Asn Thr Thr Val Asp
141          595          600          605
143 Gly Tyr Lys Val Asn Ala Asn Gly Glu Trp Val
144          610          615

```

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```

147 <210> SEQ ID NO: 2
148 <211> LENGTH: 40
149 <212> TYPE: PRT
150 <213> ORGANISM: Artificial Sequence
152 <220> FEATURE:
153 <223> OTHER INFORMATION: stabilizing strand
155 <220> FEATURE:
156 <221> NAME/KEY: MOD_RES
157 <222> LOCATION: (2)
158 <223> OTHER INFORMATION: Nle
160 <400> SEQUENCE: 2
W--> 162 Cys Xaa Gly Gly Gly Glu Ile Glu Ala Leu Lys Lys Glu Ile Glu Ala
163 1 5 10 15
165 Leu Lys Lys Glu Ile Glu Ala Leu Lys Lys Glu Ile Glu Ala Leu Lys
166 20 25 30
168 Lys Glu Ile Glu Ala Leu Lys Lys
169 35 40
171 <210> SEQ ID NO: 3
172 <211> LENGTH: 38
173 <212> TYPE: PRT
174 <213> ORGANISM: Artificial Sequence
176 <220> FEATURE:
177 <223> OTHER INFORMATION: hybrid sequence
179 <220> FEATURE:
180 <221> NAME/KEY: MOD_RES
181 <222> LOCATION: (2)
182 <223> OTHER INFORMATION: Nle
184 <400> SEQUENCE: 3
W--> 186 Cys Xaa Gly Ile Glu Glu Leu Glu Lys Lys Ile Thr Glu Leu Lys Gln
187 1 5 10 15
189 Lys Ile Asp Ala Leu Glu Asn Gln Ile His Arg Leu Glu Gln Glu Ile
190 20 25 30
192 Lys Glu Leu Asp Glu Ser
193 35
195 <210> SEQ ID NO: 4
196 <211> LENGTH: 38
197 <212> TYPE: PRT
198 <213> ORGANISM: Artificial Sequence
200 <220> FEATURE:
201 <223> OTHER INFORMATION: hybrid sequence
203 <220> FEATURE:
204 <221> NAME/KEY: MOD_RES
205 <222> LOCATION: (2)
206 <223> OTHER INFORMATION: Nle
208 <400> SEQUENCE: 4
W--> 210 Cys Xaa Gly Leu Glu Glu Ala Glu Lys Lys Ala Thr Glu Ala Lys Gln
211 1 5 10 15
213 Lys Val Asp Ala Leu Glu Asn Gln Val His Arg Leu Glu Gln Glu Leu
214 20 25 30

```

RAW SEQUENCE LISTING  
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```

216 Lys Glu Ile Asp Glu Ser
217          35
219 <210> SEQ ID NO: 5
220 <211> LENGTH: 20
221 <212> TYPE: PRT
222 <213> ORGANISM: Artificial Sequence
224 <220> FEATURE:
225 <223> OTHER INFORMATION: consensus sequence
227 <220> FEATURE:
228 <221> NAME/KEY: PEPTIDE
229 <222> LOCATION: (4)..(20)
230 <223> OTHER INFORMATION: Amino acids 4, 5, 12, 16 and 20 are Xaa wherein Xaa = any
amino
231          acid
233 <400> SEQUENCE: 5
W--> 235 Glu Glu Leu Xaa Xaa Lys Ile Asp Glu Leu Asp Xaa Glu Ile Ala Xaa
236 1          5          10          15
W--> 238 Leu Glu Lys Xaa
239          20
241 <210> SEQ ID NO: 6
242 <211> LENGTH: 8
243 <212> TYPE: PRT
244 <213> ORGANISM: Artificial Sequence
246 <220> FEATURE:
247 <223> OTHER INFORMATION: consensus sequence
249 <400> SEQUENCE: 6
251 Glu Glu Leu Ser Asp Lys Ile Asp
252 1          5
254 <210> SEQ ID NO: 7
255 <211> LENGTH: 27
256 <212> TYPE: PRT
257 <213> ORGANISM: Artificial Sequence
259 <220> FEATURE:
260 <223> OTHER INFORMATION: hybrid sequence
262 <220> FEATURE:
263 <221> NAME/KEY: MOD_RES
264 <222> LOCATION: (2)
265 <223> OTHER INFORMATION: Nle
267 <400> SEQUENCE: 7
W--> 269 Cys Xaa Gly Glu Ile Glu Ala Leu Lys Lys Lys Ile Glu Glu Leu Ser
270 1          5          10          15
272 Asp Lys Ile Asp Glu Leu Glu Lys Glu Ile Lys
273          20          25
275 <210> SEQ ID NO: 8
276 <211> LENGTH: 21
277 <212> TYPE: PRT
278 <213> ORGANISM: Haemophilus influenzae
280 <400> SEQUENCE: 8
282 Ile Lys Lys Val Leu Glu Ile Gly Leu Asn Met Ser Gln Glu Ala Ser
283 1          5          10          15

```

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```

285 Asn Leu Thr Ser Ala
286                20
288 <210> SEQ ID NO: 9
289 <211> LENGTH: 27
290 <212> TYPE: PRT
291 <213> ORGANISM: Artificial Sequence
293 <220> FEATURE:
294 <223> OTHER INFORMATION: hybrid sequence
296 <400> SEQUENCE: 9
298 Glu Ala Glu Ile Lys Lys Leu Leu Glu Ile Ile Leu Asn Leu Ser Gln
299 1                5                10                15
301 Glu Ile Ser Asn Leu Thr Ser Ala Leu Lys Gly
302                20                25
304 <210> SEQ ID NO: 10
305 <211> LENGTH: 20
306 <212> TYPE: PRT
307 <213> ORGANISM: Streptococcus pneumoniae
309 <400> SEQUENCE: 10
311 Leu Glu Lys Asp Val Glu Asp Phe Lys Asn Ser Asp Gly Glu Gln Ala
312 1                5                10                15
314 Glu Gln Val Leu
315                20
317 <210> SEQ ID NO: 11
318 <211> LENGTH: 15
319 <212> TYPE: PRT
320 <213> ORGANISM: Streptococcus pneumoniae
322 <400> SEQUENCE: 11
324 Leu Glu Asp Asn Leu Lys Asp Ala Glu Thr Asn Asn Val Glu Asp
325 1                5                10                15
327 <210> SEQ ID NO: 12
328 <211> LENGTH: 10
329 <212> TYPE: PRT
330 <213> ORGANISM: Streptococcus pneumoniae
332 <400> SEQUENCE: 12
334 Leu Ala Lys Lys Gln Thr Glu Leu Glu Lys
335 1                5                10
337 <210> SEQ ID NO: 13
338 <211> LENGTH: 35
339 <212> TYPE: PRT
340 <213> ORGANISM: Artificial Sequence
342 <220> FEATURE:
343 <223> OTHER INFORMATION: hybrid sequence
345 <400> SEQUENCE: 13
347 Asp Val Glu Asp Phe Lys Asn Ser Asp Gly Glu Leu Glu Asp Asn Leu
348 1                5                10                15
350 Lys Asp Ala Glu Thr Asn Asn Val Glu Asp Ala Lys Lys Gln Thr Glu
351                20                25                30
353 Leu Glu Lys
354                35

```

FYF

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

## VERIFICATION SUMMARY

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Input Set : A:\003592-007.ST25.txt

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:162 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:186 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:210 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:235 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:238 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:269 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:405 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
L:433 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16